

MSRRPWLLALALAVALAAGSAGASTGSATVPVATQDGPDYVFHRAHERMLFQTSY
TLENNGSVICPNNGQCFCLAWLKSNGTNAEKLAANILQWITFALSALCLMFYGYQTW
KSTCGWEIYVATIEMIKFIIEYFHEFDEPAVISSNGNKTWLRYAEWLLTCPVILIHS
NLTLGLANDYNKRTMGLLVDIGTIWGTTAALSKGYVRVIFFLMGLCYGIYTFNAAKV
YIEAYHTVPKGICRDLVRYLAWLYFCSWAMFPVLFLGPEGFGHINQFNSAIAHAILDL
ASKNAWSMMGHFLRVKIHEHILLYGDIRKKQKVNVAGQEMEVETMVHEEDDETQKV
PTAKYANRDSFIIMRDRLKEKGFFETRASLDGDPNGDAEANAAAGGKPGMEMGKMTG
MGMGMGAGMGMATIDSGRVILAVPDISMVDFREQFARLPVPYELVPALGAENTQL
VQQAQSLGGCDFVLMHPEFLRDRSPTGLPRLKMGGQRAAFGWAAIGPMRDLIEG
SGVDGWLEGPSFGAGINQQALVALINRMQQAKKMGMMGGGMGMGGGMGM
GMGMGMAPSMNAGMTGGGGASMGAVMGMGMGMQPMQQAMPAMSPMMTQ
QPSMMSQPSAMSAGGAMQAMGGVMPSPAPGGRVGTNPLFGSAPSPLSSQPGISP
GMATPPAATAAPAAGGSEAEMLQLMSEINRLKNELGE

Fig. 1A

MDYGGALSAVGRELLFVTNPVVNGSVLVPEDQCYCAGWIESRGTNQATASNVLQ
WLAAGFSIPLL MFYAYQTWKSTCGWEEIVCAIEMVKVILEFFFKNPSMLYLATGH
RVQWLRYAEWLLTCPVILIHSNLTGLSN DYSRRTMGLLVSDIGTIVWGATSAMATGY
VKVIFFCLGLCYGANTFFHAAKAYIEGYHTPKGRCRQVVTGMAWLFFVSWGMFPIL
FILGPEGFGVLSYGSTVGHTIIDLMSKNCWGLLGHYLRVLIHEHILIHGDIRTTKLNIG
GTEIEVETLVEDEAEAGAVNKGTYASRESFLVMRDKMKEKGIDVRA SLDNSKEVE
QEQAARAAMMMMNNGNGMGGMGMNGMNGMGGMNGMAGGA KPGLELTPQLQP
GRVILAVPDISMVDFREQFAQLSVTYELVPALGADNTLALVTQAQN LGGVDFVLIHP
EFLRDRSSTSILSRLRGAGQRVAAGFWAQLGP MRDLIESANLDGWLEGPSFGQQGILP
AHIVALVAKMQQMRKMQQM QQIGMMTGGMNGMGGMGGMNGMGGNGMNN
MGNGMGGMGNGMGGNGMNGMGGNGMNNMGGNGMAGNGMGGMGGNGM
GGSMNGMSSGVANVTPSAAGGMGGMNGMAAPQSPGMNGGRLGTNPLFNAA
PSPLSQLGAEAGMGSMGGMGGMSGMGGMGGMGGMGGAGAATTQAAGGNAEA
EMLQNL MNEINRLKRELGE

Fig 1B

MiptavegvsqAQITGRPEWIWLAGTALMGLGTLYFLVKGMGVSDPDAKKFYAITTLVPAIAFT
MYLSMLLGYGLTMVPFGGEQNPIYWARYADWLFTTPLLLLDALLVDADQGTILALVGADG
IMIGTGLVGALTKVYSYRFVWWAISTAAMLYILYVLFFGFTSKAESMRPEVASTFKVLRNVT
VWLWSAYPVVWLIGSEGAGIVPLNIETLLFMVLDVSAKVGFGILLRSRAIFGEAEAPEPSAG
DGAAATSD

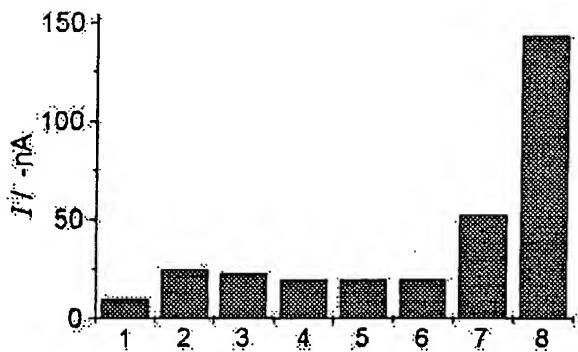
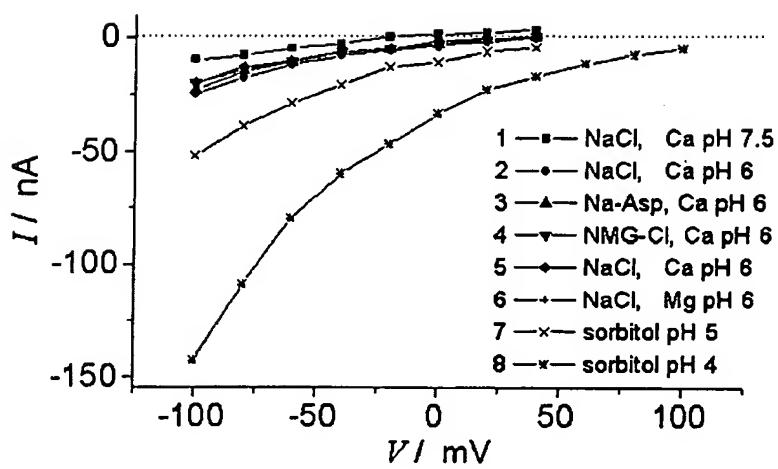
Fig. 1C

Chop1 ..	MSRRPWLLALALAVALAAGSAGASTGSATPVATQDGPDYVFRAHERMFQTSYTL	EN 60
Chop2 ..	MDYGGALS	AVGREFVTPV 23
Bop ..		M
*		
Chop1 ..	NGSVICIPNNGOCFCLAELKSN - CTVNAEKHANIDQWITPALAACCMVGYQHKSTC	118
Chop2 ..	NGCVL-VPED-CYCAGNIESR - CANGAOTHSNVQNLAAQPSIILMAYQWIKSTC	79
Bop ..	LPTAVEGVSQAITGRPEWIWLALITALMGAGTLYFLVKGMVSDPDAKEYAIITLVPA	51
* * *		
Chop1 ..	GWEETVQATHHIIKFEIYTHEDPEAVISSLNGKTVWLRKTAEHTDCTHNGHESM	178
Chop2 ..	GKCGTIVCAEVVVALELFERKNSMILATSHRVQHRYAEEAEEAEEAEEAEEAEEA	139
Bop ..	IAFTM --- LSMLGLGYGLTMVP GGEQ --- IPIYARQDWSETTPLHDIA - EL	100
* * *		
Chop1 ..	GEHNDYINKEAM - GLIVSDIGLIGVNGAASSMATGYN - KVIIECLGLCYCANRHHAS - RAK	235
Chop2 ..	GESNEYSRADM - GLIVSDIGLIGVNGAASSMATGYN - KVIIECLGLCYCANRHHAS - RAK	196
Bop ..	V-DAB-Q-GTILAVVGAEIGIMGTOLVGAETKVSYRFVWWAISTAAMLYILYVLFFGFT	157
* * *		
Chop1 ..	PEAVHTVPKGICRDLYRILAWHYRCSDAANGQPVDTLLGPPGFHINQFNSAIAHADIAS	295
Chop2 ..	PGCXTHTVPKGRCRQVVTGMAWHLFVVSAGMTRIPLIGACALLSVYGSTVGHITDPM	256
Bop ..	SKAESMRPEV -- ASTFKVIRNVTVVLWSAMPVWVIESEGAGIVPLNIETLLFMVDVSA	215
#		
Chop1 ..	KNAISMMCHFLRKVKHENEHILLYEDIRKKOKVNVAQOMEVEITMHEEDDETQKVP - RAK	354
Chop2 ..	KNCAGLLCHYERVVLHNEHILHGDIRKTTRLNIGETPIEVSTLVEDAEAGAVNKGEKG	316
Bop ..	KVGEGLI -- LERSRAIFGEAEAPEPSAGDGA - AATSD	
#		
Chop1 ..	ANPDSHIIIMRBRRLKEKIFETRASLGDPNGDABANAAAGGKPGMEMGKMTGMMGMSMGADM	414
Chop2 ..	ASKESELVMRDKMKEKGIDVRAISIANSKEVEQEQQAARRAMMMNGNGMGMMGMMNGMN	376
Chop1 ..	GMATIDS-----GRVIIIAVPEIISMVDFPREOFARLPVVPYELIVPALGADM	459
Chop2 ..	GGMNGMAGGAKPGLETPQLQPGRVIIAVPEIISMVDFPREOFQOSVTEIVPALGADM	436
#		
Chop1 ..	IQIVOCACSLGGCCDFVIMHRPEFLDRSPTGLESPIKMGCCRRAATG - RAIQHMRDLTBSG	519
Chop2 ..	LAIWTCAGCNLCGVDFVLIHRPEFLDRSSTSISRSIRGACCRRAATG - QLQHMRDLTBSA	496
Chop1 ..	GVDGWLECPSEFGAGINQOALVALINRMOCACKMGMC - - - GMGCMGCGCG-N	568
Chop2 ..	NLDGWLECPSEFGCGTLPAHIVALVAKNOOMRIGMOQQIGMMTGGMNGGGMCGCG-N	556
Chop1 ..	GMGCMG - MAPSMNAGCTGGCG -- ASMGK - - - AVMMGNGMQPHQAMP -- AMSPM	616
Chop2 ..	GGGNGNNMNGNGGCGNGNCNGMNGMGGNGNMNNMGGNGAGNGMGGGGNGNGGGS	616
#		
Chop1 ..	MTQQPS - MMSQPSAMSACIAMQAMGGVMPSPAP - - - CGRVETNPLEGSAPSPLSSG - - -	667
Chop2 ..	MNGMSSGVVANVTPSAAGGGMGGMNGGMAAPQSPGMNGRLLGTNPLENAAPSPLSSOLGA	676
Chop1 ..	- PGIISPGMATPPAATAAPRAGSFAEMIQQLMSEINRLN - EIGEK	712
Chop2 ..	EAGMGSMMGGMGGMSGMGGMGGMGGAGAATTQAAAGCNAAPMIONLMNEINRLKRELGK	737

Fig. 1D



Fig. 2

a**b****Fig. 3**

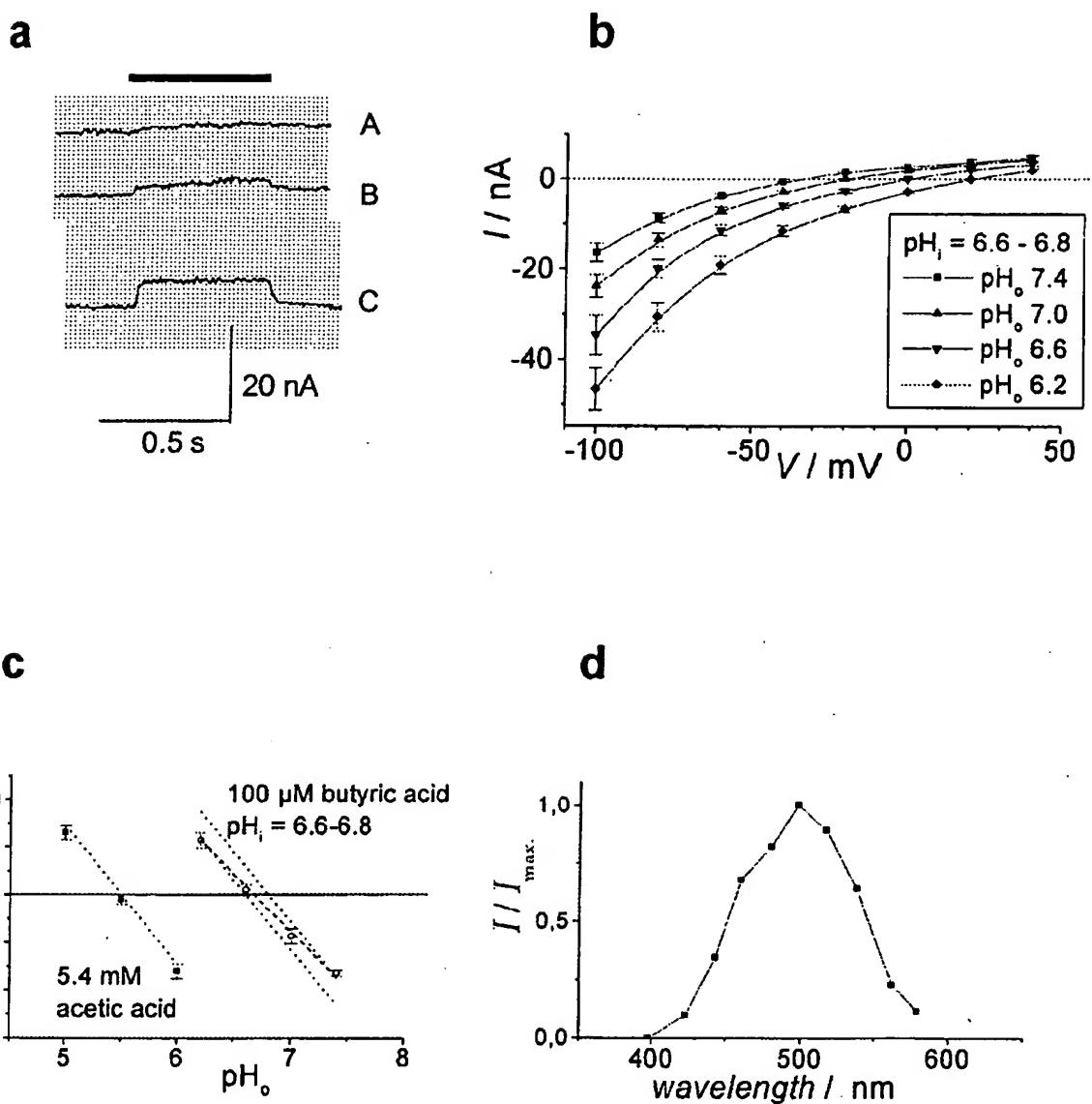


Fig. 4